

[illegible]

```

A4.6.1  WINTYTGEPTYAADEKRRFTFSLETSASTAYLQISNLKNDDTATYFCAK
          * *          *** **      * *
F(ab)-12 WINTYTGEPTYAADEKRRFTFSLDTSKSTAYLQMNSLRAEDTAVYYCAK
          * * * * * * * * * * * * * *
humIII   VISG DGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR
          50  a          60          70          80  abc          90

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**Fig. 1A**

Z4.6.1      YPHYYGSSHWYFDVWGAGTTVTVSS (SEQ ID NO:9)  
                              \*     \*  
F(ab)-12    YPHYYGSSHWYFDVWGQGTLVT VSS (SEQ ID NO:7)  
                              \*     \*  
humIII      G-----FDYWGQGT LVT VSS (SEQ ID NO:11)

110

## Variable Light

A4.6.1      DIQMTQTSSLSASLGDRVIISCSASODISNYLNWYQQKPDGTVKVLIIY  
                  \*\*                   \*                   \*                   \*                   \*\*\*\*  
 F(ab)-12    DIQMTQSPSSLSASVGDRTITCSASODISNYLNWYQQKPGKAPKVLIIY  
    \*                   \*                   \*                   \*  
 humKI        DIQMTQSPSSLSASVGDRTITCRASQSIISNYLAWYQQKPGKAPKLLIIY  
                  1                   10                   20                   30                   40

**Fig. 1B**

A4.6.1      **FTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYYCOOYSTVPWTF**  
   \*\*       \*     \*     \*

F(ab)-12    **FTSLHSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCOOYSTVFWTF**  
                 \*\*     \*   \*\*\*

humKI  
30                60                70                80                90  
**AASSLESGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQYNPLPWTF**

A4.6.1 GGGTKI<sup>\*</sup>EIKR (SEQ ID NO: 10)  
F(ab)-12 GQG<sup>\*</sup>TKVEIKR (SEQ ID NO: 8)  
humKI GQG<sup>\*</sup>TKVEIKR (SEQ ID NO: 12)  
100

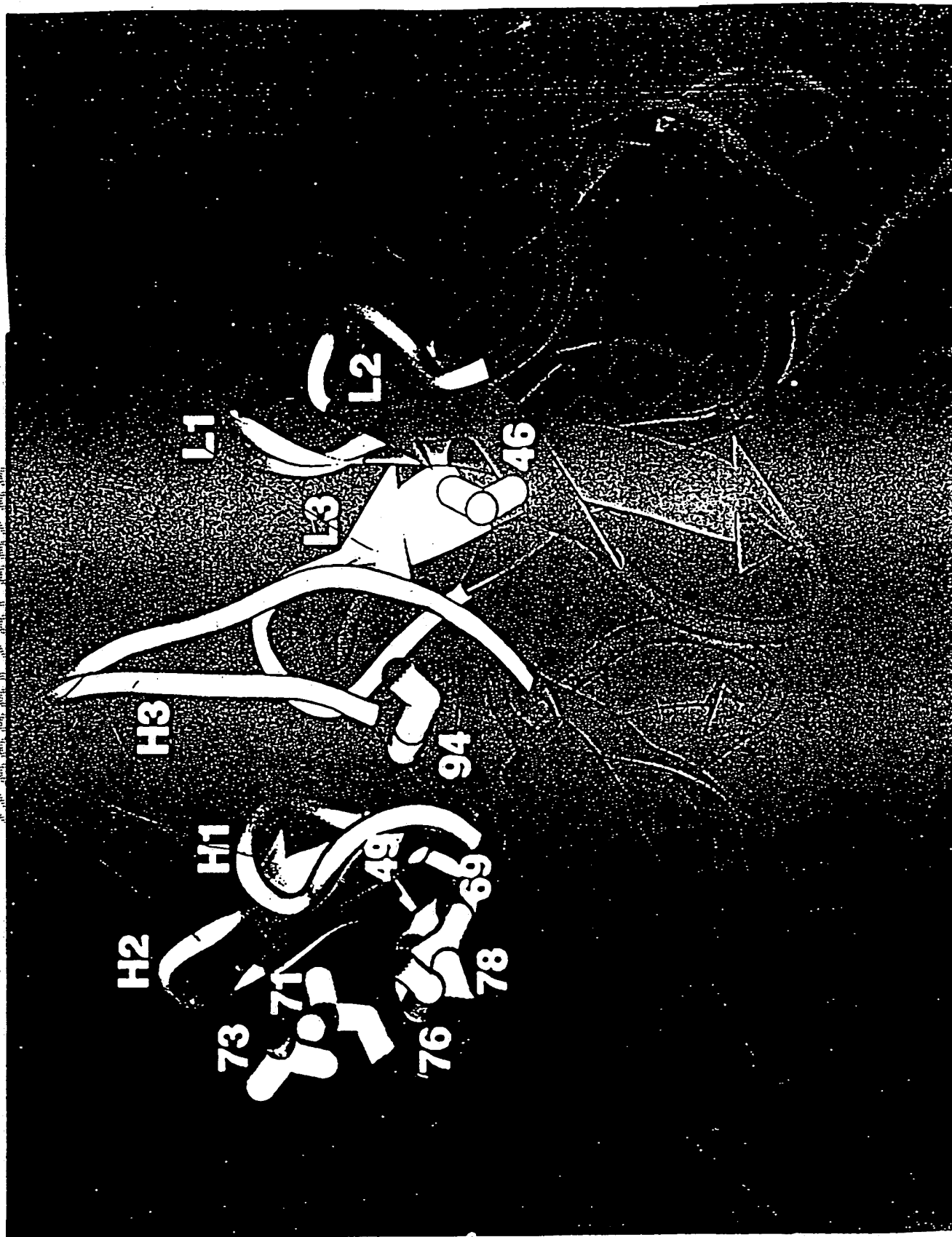


Fig. 2

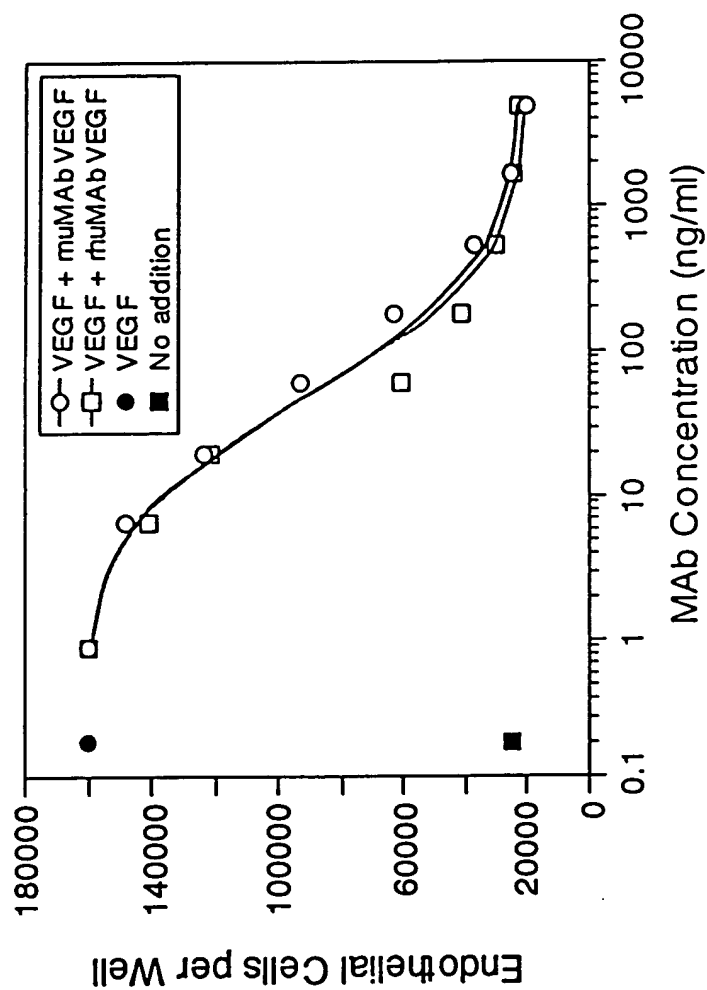


Fig. 3

269030.69430630

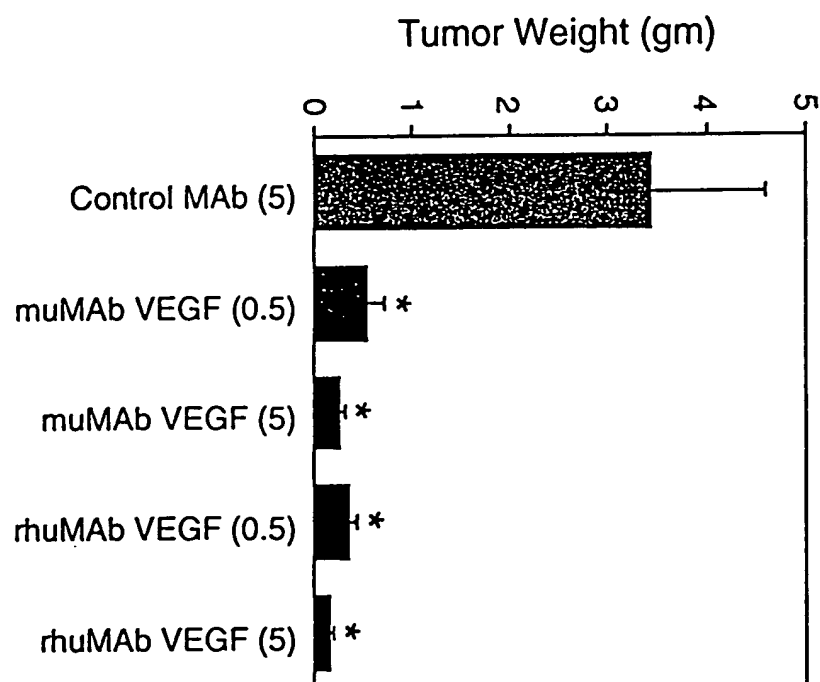


Fig. 4

# V<sub>L</sub> domain

	10	20	30	40
A4.6.1	DIQMTQTSSSLASLGDRVIISCSASQDISNYLNWYQQKP			
	**	*	* *	
hu2.0	DIQMTQSPSSLSASVGDRTITCSASQDISNYLNWYQQKP			
hu2.10	DIQMTQSPSSLSASVGDRTITCSASQDISNYLNWYQQKP			

Fig. 5A

	50	60	70	80
A4.6.1	DGTVKVLIIYFTSSLHSGVPSRFSGSGSGTDYSLTISNI·EP			
	**** *		** *	*
hu2.0	GKAPKLLIYFTSSLHSGVPSRFSGSGSGTDFTLTISLQP			
hu2.10	GKAPKLLIYFTSSLHSGVPSRFSGSGSGTDYTLTISLQP			

	90	100
A4.6.1	EDIATYYCQYSTVPWTFGGGKLEIK (SEQ ID NO:10)	
	*	* *
hu2.0	EDFATYYCQYSTVPWTFGQGTKVEIK (SEQ ID NO:13)	
hu2.10	EDFATYYCQYSTVPWTFGQGTKVEIK (SEQ ID NO:15)	

# - V<sub>H</sub> domain

	10	20	30	40
A4.6.1	EIQLVQSGPELKQPGETVRISCKASGYTFTNYGMNWVKQA			
	* * * * *	* * *		*
hu2.0	EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVRQA			
hu2.10	EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWIRQA			

Fig. 5B

	50 a	60	70	80
A4.6.1	PGKGLKWMGWINTYTGEPTYAADFKRRFTFSLETSASTAYL			
	* *		* * * * *	
hu2.0	PGKGLEWVGWINTYTGEPTYAADFKRRFTISRDNKNTLYL			
hu2.10	PGKGLEWVGWINTYTGEPTYAADFKRRFTISLDTSASTVYL			

	abc	90	100abcdef	110
A4.6.1	QISNLKNDdTATYFCAKYPHYYGSSHWYFDVWGAGTTVTVSS (SEQ ID NO:9)			
	*** **	* * *		* *
hu2.0	QMNSLRAEDTAVYYCARYPHYYGSSHWYFDVWGQGLTVTVSS (SEQ ID NO:14)			
hu2.10	QMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGLTVTVSS (SEQ ID NO:16)			

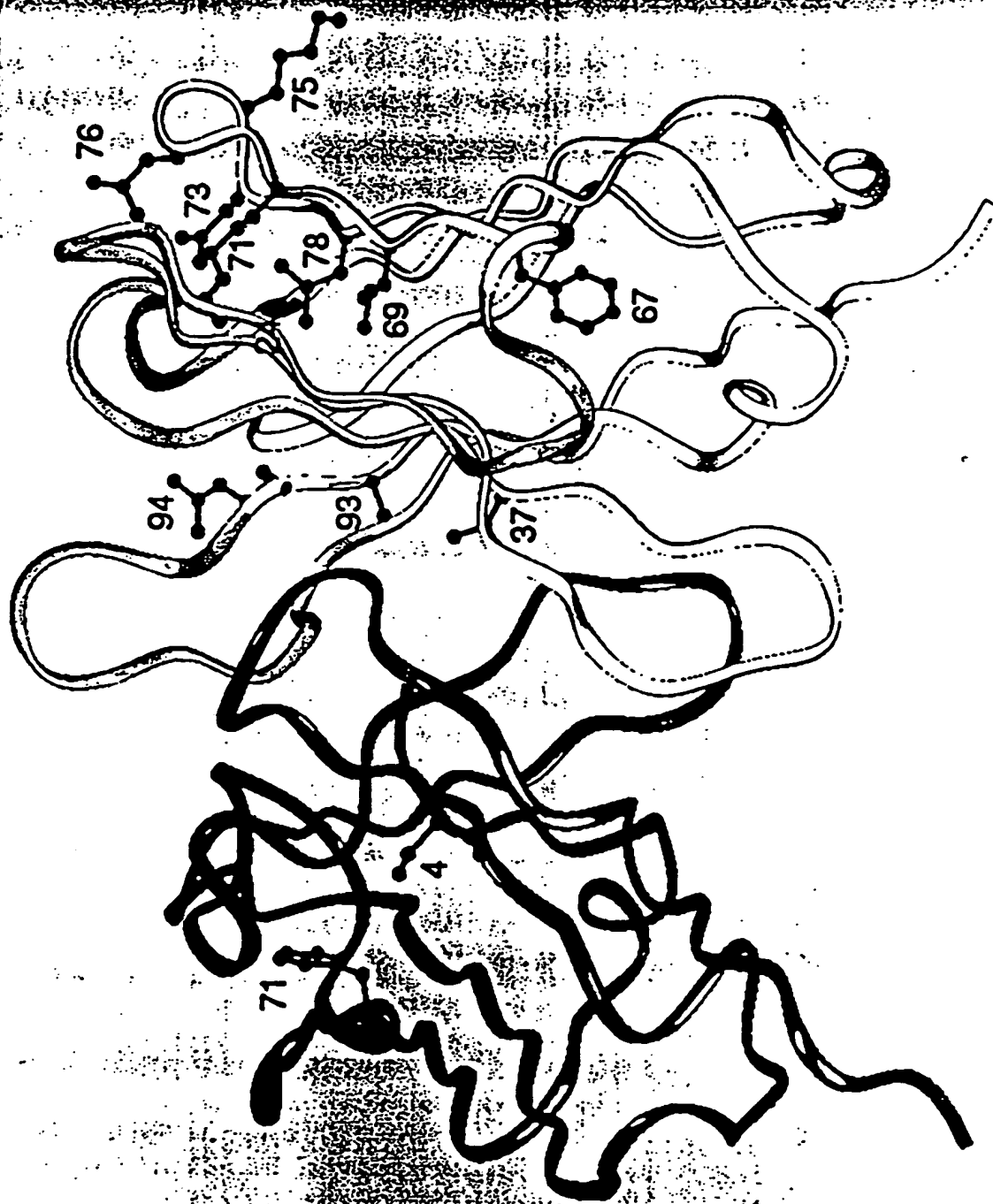
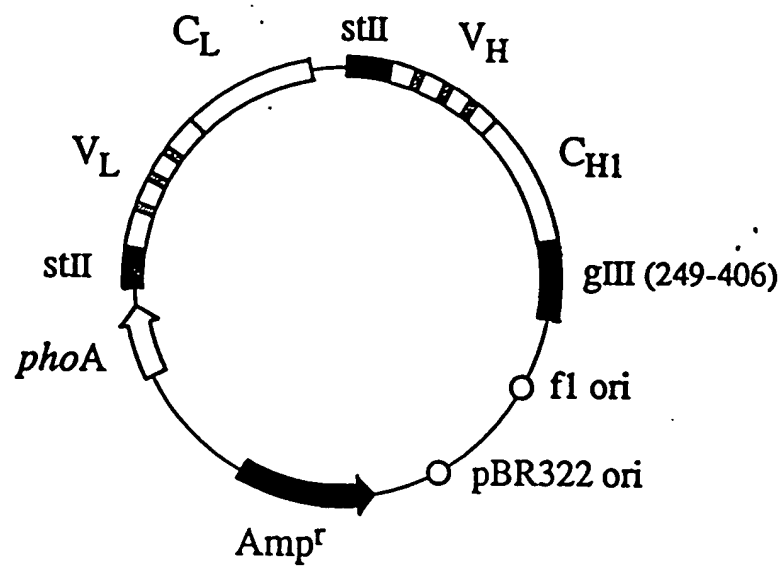


Fig. 6



Transform *E. coli*

+ M13KO7 helper phage

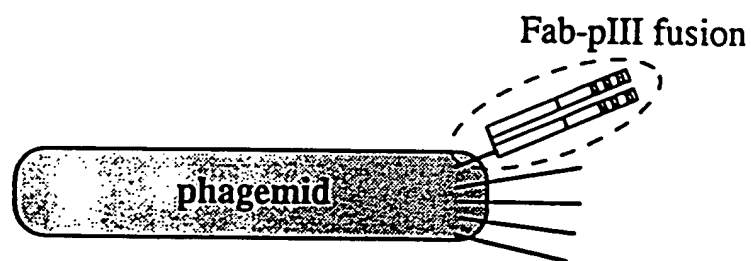


Fig. 7

1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTATTATTT AAGCTTTTGA GATTATCGTC ACTGCAATGC  
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACCT CTAATAGCAG TGACGTTACG

101 TTCGCAATAT GCGGCAAAAT GACCAACAGC GGTGATTGA TCAGGTAGAG GGGGCGCTGT ACAGAGTAA GCGCGATGCC AGCATTCCTG ACAGCGATAC  
AAGCGTTATA CCGCGTTTA CTGGTTGTC CCAACTAACT AGTCCATCTC CCGCGGACA TGCTCCATT CCGGCTACGG TCGTAAGGAC TGCTGCTATG

201 GGAGCTGCTG CGCGATTACG TAAAGAAGTT ATTGAAGCAT CCTCGTCAGT AAAAAGTTAA TCTTTTCAAC AGCTGTCATA AAGTTGTAC GCGCGAGACT  
CCTCGACGAC GCGCTAATGC ATTTCTTCAA TAACTTCGTA GGAGCAGTCA TTTTCAATT AGAAAAAGTTG TCGACAGTAT TTCAACAGTG CCGGCTCTGA

301 TATAGTCGCT TTGTTTTTAT TTTTAAATGT ATTTGTAATCT AGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGGTTGA GGTGATTTTA TGA AAAAAGAA  
ATATCAGCGA AACAAAAATA AAAAATTACA TAAACATTGA TCTTAAGCTC GAGCCATGGG CCCCTAGGAG ATCTCCAAT CCACTAAAAT ACTTTTCTT  
M etLysLysAsn  
-23 Begin still signal sequence

401 TATCGCATTT CTTCTTGCAT CTATGTTTCTG TTTTCTTATT GCTACAAAACG CGTACGCTGA TATCCAGTTG ACCAGTCCC CGAGCTCCCT GTCCGCTCT  
ATAGCGTAAA GAAGAACGTA GATACAAGCA AAAAAGATAA CGATGTTTGC GCATGCGACT ATAGGTCAAC TGGGTCAGGG GCTCGAGGGA CAGGCGGAGA

-19 IleAlaPhe LeuLeuAlaSer erMetPheVa lPheSerIle AlaThrAsnA lATyrAlaAs pileGlnLeu ThrGlnSerP roSerSerLe userAlaSer  
Begin light chain

501 GTGGGCGATA GGGTCACCAT CACCTGCAGC GCAAGTCAGG ATATTAGCAA CTATTAAAC TGGTATCAAC AGAAACCAGG AAAAGTCCG AAACACTACTGA  
CACCCGCTAT CCCAGTGGTA GTGGACGTCG CGTTCAGTCC TATAATCGTT GATAAATTG ACCATAGTTG TCTTTGGTCC TTTTCGAGGC TTTGATGACT

15 ValGlyAspA rgValThrIl eThrCysSer AlaSerGlnA spIleSerAs nTyrLeuAsn TrpTyrGlnG lNlysProGl yLysAlaPro LysLeuLeuLeu

601 TTTACTTCAC CTCCTCTCTC CACTCTGGAG TCCCTTCTCG CTTCTCTGGA TCCGGTTCTG GGACGGATTA CACTCTGACC ATCAGCAGTC TGCAGCCAGA  
AAATGAAGTG GAGGAGAGAG GTGAGACCTC AGGGAAGAGC GAAGAGACCT AGGCAAGAC CTGCGCTAAT GTGAGACTGG TAGTCGTGAG ACGTCGGTCT

49 TyrPheTh rSerSerLeu HisSerGlyV alProSerAr gPheSerGly SerGlySerG lyThrAspTy rThrLeuThr ileSerSerL euGlnProGlu

701 AGACTTCGCA ACTTATTACT GTCAACAGTA TAGCACCGTG CCGTGGACGT TTGGACAGGG TACCAAGGTG GAGATCAAAAC GAACGTGTGC TGCACCATCT  
TCTGAAGCGT TGAATAATGA CAGTTGTGAT ATCGTGGCAC GGCACCTGCA AACCTGTCCC ATGGTTCCAC CTCTAGTTG CTTGACACCG ACGTGGTAGA

82 AspPheAla ThrTyrTyrC ysglnGlnTy rSerThrVal ProTrpThrP heglyGlnGl yThrLysVal GluileLysA rgThrValAl aAlaProSer

801 GTCTTCATCT TCCCGCCATC TGATGAGCAG TTGAAATCTG GAACCTGCTC TGTGTGTGTC CTGCTGAATA ACTTCTATCC CAGAGAGGCC AAAGTACAGT  
CAGAAAGTAG AGGCGGTAG ACTACTCGTC AACTTTAGAC CTTGACGAAG ACAACACACG GACGACTTAT TGAAGATAGG GTCTCTCCGG TTTCATGTCA

115 ValPheIleP heProProSe rAspGluGln LeuLysSerG lyThrAlase rValValCys LeuLeuAsnA snPheTyrPr oArgGluAla LysValGlnTrp

901 GGAAGGTGGA TAAACGCCCTC CAATCGGGA ACTCCAGGA GAGTGTACA GAGCAGGACA GCAAGGACAG CACCTACAGC CTCAGCAGCA CCTGACGCT  
CCTCCACCT ATTGCGGAG GTTAGCCCAT TGAGGTCCT CTCACAGTGT CTCGTCTGT CGTTCCTGTG GTGATGTGCG GAGTCGTCT GGGACTGCGA

149 LysValas pasnAlaLeu GlnSerGlyA snSerGlnGl uSerValThr GluGlnAspS erLysAspSe rThrTyrSer LeuSerSerT hrLeuThrLeu

1001 GAGCAAGCA GACTACGAGA AACACAAAGT CTACGCCCTG GAAGTCACCC ATCAGGGCCT GAGCTCGCCC GTCACAAAAGA GCTTCAACAG GGGAGAGTGT  
CTCGTTTCTG CTGATGCTCT TTGTGTTTCA GATGCGGACG CTTCAAGTGG TAGTCCCGA CTCGAGCGGG CAGTGTCTT CCAAGTTGTC CCTCTCACA

182 SerLysAla AspTyrGluL yshisLysVa ltyrAlaCys GluValThrH isGlnGlyLe uSerSerPro ValThrLysS erPheAsnAr gGlyGluCys

Fig. 8A



1101 TAAGCTGATC CTCTACGCCG GACGCATCGT GGCCCTAGTA CGCAACTAGT CGTAAAGG GATCTAGAG GTTGAGGTGA TTTTATGAAA AAGAATATCG  
 ATTCGACTAG GAGATCGGC CTGCGTAGCA CCGGGATCAT GCGTTGATCA GCAATTTTCC CATAGATCTC CAACTCCACT -23 MetLys LysAsnIleAla  
 215 OC\*  
 1201 CATTCTTCT TGCATCTATG TTCGTTTTTT CTATTGCTAC AAACGCGTAC GCTGAGGTTC AGCTGGTGA GTCTGGCGGT GGCCTGGTGC AGCCAGGGGG  
 GTAAAGAAGA ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGCGCATG CGACTCCAAG TCGACCACTT CAGACCGCCA CCGGACCACG TCGGTCCCCC  
 -17 PheLeuLe uAlaSerMet PheValPheS erIleAlaTh rAsnAlaTyr AlaGluValG InLeuValG1 userGlyGly GlyLeuValG InProGlyGly  
 1301 CTCACCTCCGT TTGCTCTGTG CAGCTTCTGG CTATACCTTC ACCAACTATG GTATGAACCTG GATCCGTGAC GCGCCCGGTA AGGGCCCTGGA ATGGGTGGA  
 GAGTGAGGCA AACAGGACAC GTCGAAGACC GATATGGAAG TGGTTGATAC CATACTTGAC CTAGGAGTC CCGGGCCCCAT TCCCGGACCT TACCCAACCT  
 17 SerLeuArg LeuSerCysA laAlaSerG1 yTyrThrPhe ThrAsnTyrG lYMetAsnTr pileArgGln AlaProGlyL ySGlyLeuG1 utrPvalGly  
 1401 TGGATTAAACA CCTATACCGG TGAACCGACC TATGCTGCGG ATTTCAAACG TCGTTTTACT ATATCTGCAG ACACCTCCAG CAACACAGTT TACCTGCAGA  
 ACCTAATTGT GGATATGGCC ACTTGCTGG ATACGACGCC TAAAGTTTGC AGCAAAATGA TATAGACGTC TGTGAGGTC GTTGTGTCAA ATGGACGTCT  
 50 TrpIleAsnT hrTyrThrG1 yGluProThr TyrAlaAlaA spPheLysAr gArgPheThr ileSerAlaA spThrSerSe rAsnThrVal TyrLeuGlnMet  
 1501 TGAACAGCCT GCGCGCTGAG GACACTGCCG TCTATTACTG TGCAAAAGTAC CCGCACTATT ATGGGAGCAG CCACTGGTAT TTCGACGTCT GGGGTCAAGG  
 ACTTGTCGGA CCGCGGACTC CTGTGACGGC AGATAATGAC ACGTTTCATG GCGGTGATAA TACCCTCGTC GGTGACCCATA AAGCTGCAGA CCCCAGTTCC  
 84 AsnSerLe uArgAlaGlu AspThrAlav alTyrTyrCy salaLysTyr ProHisTyrT yRGlySerSe rHisTrpTyr PheAspValt rpGlyGlnGly  
 1601 AACCTGGTC ACCGTCTCCT CGGCCTCCAC CAAGGGCCCA TCGGTCTTCC CCCTGCCACC CTCCTCCAAG AGCACTCTG GGGGCACAGC GGCCCTGGGC  
 TTGGGACCAG TGGCAGAGGA GCGGAGGTG GTTCCCGGT AGCCAGAAG GGGACCGTG GAGGAGTTC TCGTGGAGC CCCCCTGTGC CCGGGACCCG  
 117 ThrLeuVal ThrValSers erAlaSerTh rLysGlyPro SerValPheP roLeuAlaPr oSerSerLys SerThrSerG lyGlyThrAl aAlaLeuGly  
 1701 TGCCTGGTCA AGGACTACTT CCCCGAACCG GTGACGGTGT CGTGGAACCTC AGCGCCCTG ACCAGCGCG TGCACACCTT CCGGCTGTC CTACAGTCTT  
 ACGGACCAGT TCCTGATGAA GGGCTTGGC CACTGCCACA GCACCTGAG TCCGCGGAC TGGTCCCGC ACGTGTGAA GGGCCGACAG GATGTGAGGA  
 150 CysLeuVal lYsAspTyrPh eProGluPro ValThrValS erTrpAsnSe rGlyAlaLeu ThrSerGlyV alHisThrPh eProAlaVal LeuGlnSerSer  
 1801 CAGGACTCTA CTCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA  
 GTCCTGAGAT GAGGGAGTCG TCGCACCACT GGCACGGGAG GTCGTCGAAC CCGTGGGTCT GGATGTAGAC GTTGCACTTA GTGTTGGGT CGTTGTGGTT  
 184 GlyLeuTy rSerLeuSer SerValValt hrValProse rSerSerLeu GlyThrGlnT hrTyrIleCy sAsnValAsn HisLysProS erAsnThrLys  
 1901 GGTGACACAAG AAAGTTGAGC CCAATCTTG TGACAAAACCT CACCTCTAGA GTGGCGGTGG CTCTGGTTCC GGTGATTTTG ATTATGAAA GATGGCAAAC  
 CCAGCTGTTT TTTCAACTCG GGTTTAGAAC ACTGTTTGA GTGGAGATCT CACCGCCACC GAGACCAAAG CCACTAAAAC TAATACTTTT CTACCGTTTG  
 217 ValAspLys LysValGluP roLysSerCy sAspLysThr HisLeuAM\*S erGlyGlyG1 ySerGlySer GlyAspPheA spTyrGluLy sMetAlaAsn  
 2001 GCTAATAAGG GGGCTATGAC CGAAAATGCC GATGAAAACG CGCTACAGTC TGACGCTAAA GGCAAAACCTG ATTCTGTCG TACTGATTAC GGTGCTGCTA  
 CGATTATTCC CCCGATACTG GCTTTTACGG CTACTTTTGC GCGATGTCAG ACTGCGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT  
 250 AlaAsnLysG lYalaMetTh rGluAsnAla AspGluAsnA laLeuGlnSe rAspAlaLys GlyLysLeuA spSerValAl aThrAspTyr GlyAlaAlaIle  
 2101 TCGATGGTTT CATTGGTGAC GTTTCGGGC TTGCTAATGG TAATGGTGCT ACTGGTGATT TTGCTGGCTC TAATTCCTAA ATGGCTCAAG TCGGTGACGG  
 AGCTACC2AA GTAACCACTG CAAAGGCCG CAAAGGCCG AACGATTACC ATTACCACGA TGACCACTAA AACGACCGAG ATTAAGGTTT TACCGAGTTC AGCCACTGCC  
 284 AspGlyPh eIleGlyAsp ValSerGlyL euAlaAsnG1 yAsnGlyAla ThrGlyAspP heAlaGlySe rAsnSerGln MetAlaGlnV alGlyAspGly  
 2201 TGATAATTCA CCTTTAATGA ATAATTTCCG TCAATATTTA CCTTCCCTCC CTCAATCGGT TGAATGTCGC CCTTTTGTCT TTAGCGCTGG TAAACCATAT  
 ACTATTAGT GGAAATTACT TATTAAAGGC AGTTATAAT GGAAGGAGG GAGTTAGCCA ACTTACAGCG GGAAAACAGA AATCGCGACC AATTGGTATA  
 317 AspAsnSer ProLeuMeta snAsnPheAr gGlnTyrLeu ProSerLeuP roGlnSerVa lGluCysArg PropheValP heSerAlaG1 yLysProTyr

Fig. 8B

00/908, 469

2301 GAATTTTCTA TTGATTGTGA CAAAATAAAC TTATTCCGTG GTGTCTTTGC GTTCTTTTA TATGTTGCCA CCTTTATGTA TGTATTTTCT ACCTTTGCTA  
 CTTAAAAGAT AACTAACACT GTTTTATTG AATAAGGCACTTACAGAAACCGGCAATAGGAAATATATAGAACCGGT GGAATAACAT ACATAAAGA TGCAAACGAT  
 350 GluPheSerI leAspCysAs pLysileAsn LeupheArgG lyValPheAl aPheLeuLeu TyrValAlat hrPheMetTy rValPheSer ThrPheAlaAsn  
 2401 ACATACTGCG TAATAAGGAG TCTTAATCAT GCCAGTTCTT TTGGCTAGCG CCGCCCTATA CCTTGTCTGC CTCCCGCGGT TGCCTCGCGG TGCATGGAGC  
 TGTATGACGC ATTATTCTC AGAATTAGTA CCGTCAAGAA AACCGATCGC GCGGGGATAT GGAACACAGCG GAGGGGCGCA ACGCAGCGCC ACGTACCTCG  
 384 IleLeuAr gasnLysGlu SerOC\* (SEQ ID NO: 100)  
 2501 CGGGCCACCT CGACCTGAAT GGAAGCCGCG GCACCTCGC TAACGGATTG ACCACTCCAA GAATTGGAGC CAATCAATTC TTGCGGAGAA CTGTGAATGC  
 GCGCGGTGGA GCTGGACTTA CCTTCGGCGC CCGTGGAGCG ATTGCCTAAG TGGTGAGGTT CTTAACCTCG GTTAGTTAAG AACGCCTCTT GACACTTACG  
 2601 GCAAAACCAAC CCTTGGCAGA ACATATCCAT CGCGTCCGCC ATCTCCAGCA GCCGCACGCG GCGCATCTCG GGCAGCGTTG GGTCTGGCC ACGGGTGGCG  
 CGTTTGGTTG GGAACCGTCT TGTATAGGTA GCGCAGGCGG TAGAGGTCTG CCGCGTGGCG CCGTCCGAAC CCAGGACCGG TGCCACGCG  
 2701 ATGATCGTGC TCCTGTCTGTT GAGGACCCCG CTAGGCTGGC GGGGTTGCCT TACTGGTTAG CAGAATGAAT CACCGATACG CGAGCGAAGC TGAAGCGACT  
 TACTAGCACG AGGACAGCAA CTCCTGGGCC GATCCGACCG CCCCAACGGA ATGACCAATC GTCTTACTTA GTGGCTATGC GCTCGCTTGC ACTTCGCTGA  
 2801 GCTGCTGCAA AACGCTCTGC ACCTGAGCAA CAACATGAAT GGTCTTCGGT TTCCGTGTTT CGTAAAGTCT GGAACCGCGG AAGTCAGCGC CCTGCACCAT  
 CGACGACGTT TTGCAGACGC TGGACTCGTT GTTGTACTTA CCAGNAGCCA AAGGCACAAA GCATTTTCTG CTTTTGCGCC TTCAGTCCGG GGACGTGGTA  
 2901 TATGTTCCGG ATCTGCATCG CAGGATGCTG CTGGCTACCC TGTGGAACAC CTACATCTGT ATTACGAG CGCTGGCATT GACCCTGAGT GATTTTCTC  
 ATACAAGGCC TAGACGTAGC GTCCTACGAC GACCGATGGG ACACCTTGTG GATGTAGACA TAATTGCTTC GCGACCGTAA CTGGGACTCA CTAATAAAGAG  
 3001 TGGTCCCGCC GCATCCATAC CGCCAGTTGT TTACCTCTAC AACGTTCCAG TAACCGGGCA TGTTTCATCAT CAGTAACCCG TATCGTGAGC ATCCTCTCTC  
 ACCAGGGCGG CGTAGGTATG GCGGTCAACA AATGGGAGTG TTGCAAGGTC ATTGGCCCGT ACAAGTAGTA GTCATTTGGC ATAGCACTCG TAGGAGAGAG  
 3101 GTTTCATCGG TATCATTACC CCCATGAACA GAAATTCCCC CTTACACGGA GGCATCAAGT GACCAACACG GAATAAACCG CCTTAAACAT GGCCCGCTTT  
 CAAAGTAGCC ATAGTAATGG GGGTACTTGT CTTTAAAGGG GAATGTGCTT CCGTAGTTCA CTGGTTTGTG CTTTTTTGGC GGAATTTGTA CCGGGCGAAA  
 3201 ATCAGAAGCC AGACATTAAAC GCTTCTGGAG AAACCTCAACG AGCTGGACGC GGATGAACAG GCAGACATCT GTGAATCGCT TCACGACCCAC GCTGATGAGC  
 TAGTCTTCGG TCTGTAAATG CGAAGACCTC TTTGAGTTGC TCGACCTGCG CCTACTTGTG CGTCTGPAGA CACTTAGCGA AGTGCTGGTG CGACTACTCG  
 3301 TTTACCGCAG GATCCGGAAA TTGTAAACGT TAATATTITG TTAAATTCG CGTTAAATTT TGTTAAATC AGCTCATTTT TTAACCAATA GGCCGAAAATC  
 AAATGGCGTC CTAGGCCCTT AACATTGTGA ATTATAAAAC AATTITAAGC GCAATTAAAC TGTTAAATC AGCTCATTTT TCGAGTAAAA AATTGGTTAT CCGGCTTTAG  
 3401 GGCAAAATCC CTTATAAATC AAAAGAATAG ACGGAGATAG GGTGAGTGT TGTCCAGTT TGGAAACAAGA GTCCACTATT AAAGAACGCTG GACTCCAACG  
 CCGTTTATGG GAATATTAG TTTTCTTATC TGGCTCTATC CCAACTCACA ACAAGGTCAA ACCTTGTCTT CAGGTGATAA TTTCTTGCAC CTGAGGTTGC  
 3501 TCAAGGGCGG AAAAACCGTC TATCAGGGCT ATGGCCCACT ACGTGAACCA TCACCTTAAT TCAGTTTCTT GGGGTGAGG TGCCGTAAAG CACTAAATCG  
 AGTTTCCCGC TTTTGGCAG ATAGTCCCGA TACCGGGTGA TGCACTTGGT AGTGGATTA GTTCAAAAAA CCCCAGCTCC ACGGCATTTT GTGATTTAGC  
 3601 GAACCCCTAA GGGAGCCCC GATTAGAGC TTGACGGGGA AAGCCGGCGA ACGTGGCGAG AAAGGAAGGG AAGAAAGCGA AAGGAGCGGG CGCTAGGGCG  
 CTTGGGATTT CCCTCGGGGG CTAATCTCG AACTGCCCTT TTCGGCCGCT TGCACCGCTC TTTCTTCTCC TTTCTTCTCGT TTCTCTGCCC GCGATCCCGC  
 3701 CTGGCAAGTG TAGCGGTCAC GCTGCGCGTA ACCACCACAC CCGCCCGGCT TAATGCCCGG CTACAGGGCG GTCCTGGATC CTGCTCTGCG CGTTTCGGTG  
 GACCGTTTAC ATCGCCAGTG CGACGCGCAT TGGTGGTGTG GCGCGCGCGA ATTACCGGCG GATGTCCCGG GCAGGAGCGG GACGAGCGCG GCAAAGCCAC  
 3801 ATGACGGTGA AAACCTCTGA CACATGCAGC TCCCGGAGAC GGTACACAGT TGTCTGTAAG CCGATGCCCG GAGCAGACAA GCCCGTCCAG GCGCGTCCAG  
 TACTGCCACT TTTGGAGACT GTGTACGTG AGGCCCTCTG CCAGTGTGCA ACAGACATTC GCCTACGGCC CTCGTCTGTT CCGGCGAGTCC CCGCGCAGTC

Fig. 8C

3901 GGGTGTGGC GGGTGTGGG GCGCAGCCAT GACCCAGTCA CGTAGCGATA GCGGAGTGTG TACTGGCTTA ACTATGCGGC ATCAGAGCAG ATTGTACTGA  
 CCCACAACCG CCCACAGCCC CGCGTCGGTA CTGGGTGAGT GATGGCTAT GGGCTGAGT ATGACCGAAT TGATACGCCG TAGTCTCGTC TAACATGACT

4001 GAGTGCACCA TATGCGGTGT GAAATACCGC ACAGATGCGT AAGGAGAAAA TACCGCATCA GCGGCTCTTC CGCTTCCTCG CTCACTGACT CGCTGCGCTC  
 CTCACGTGGT ATACGCCACA CTTTATGGCG TGCTACGCA TTCCTCTTTT ATGGCGTAGT CCGCGAGAAG GCGAAGGAGC GAGTGACTGA GCGACGCGAG

4101 GGTGCTTCGG CTGCGGGCGAG CCGTATCAGC TCACTCAAAG GCGGTAATAC GGTATCCAC AGAATCAGGG GATAACGCAG GAAAGAACAT GTGAGCAAAA  
 CCAGCAAGCC GACGCGCTC GCCATAGTCG AGTGAGTTTC CGCCATTATG CCAATAGGTG TCTTAGTCCC CTATTGGGTC CTTTCTTGTA CACTCGTTTT

4201 GGCCAGCAAA AGCCAGGAA CCGTAAAAAG GCGCGTTTC TGGCGTTTTT CCATAGGCTC CGCCCCCTCG ACAGAGCATCA CAAAAATCGA CGCTCAGTC  
 CCGGTCGTTT TCGGTCCTT GGCATTTTC CGGCGCAACG ACCGCAAAA GGTATCCGAG GCGGGGGAC TGCTCGTAGT GTTTTAGCT GCGAGTTTCAG

4301 AGAGGTGGC AAACCCGACA GGAATATAA GATACCAGG GTTCCCTTTC GGAAGCTCCC TCGTGGCTC TCCTGTTCCG ACCCTGCCG TTACCGGATA  
 TCTCCACCGC TTGCGCTGT CCGATATTT CTATGGTCCG CAAAGGGGA CCTTCGAGG AGCACGGAG AGGACAAGG TGGACGGCG AATGGCCTAT

4401 CCTGTCCGC TTCTCCCTT CCGGAAGCGT GCGCTTTCT CATAGCTCAC GCTGTAGGTA TCTCAGTTTC GTGTAGGTCG TTCGCTCCAA GCTGGGCTGT  
 GGACAGGCGG AAAGAGGGA GCCCTTCGA CCGCGAAGA GTATCGAGTG CGACATCCAT AGAGTCAAGC CACATCCAGC AAGCGAGGT CGACCCGACA

4501 GTGCACGAAC CCCCCTTCA GCGGACCGC TCGGCTTAT CCGGTAACTA TCGTCTTGAG TCCAAACCCG TAAGACACGA CTTATCGCCA CTGGCAGCAG  
 CACGTGCTTG GGGGSCAGT CCGGCTGGC ACGCGGAATA GGCCATTGAT AGCAGAACTC AGGTGGGCC ATTCTGTGCT GAATAGCGGT GACCGTCGTC

4601 CCACTGGTAA CAGGATTAGC AGAGCGAGGT ATGTAGGCGG TGCTACAGAG TTCTTGAAGT GGTGGCCTAA CTACGGCTAC ACTAGAAAGA CAGTATTTGG  
 GGTGACCATT GTCCTAATCG TCTCGTCCA TACATCCGCC ACGATGTCTC AAGAACTTCA CCACCGGATT GATGCCGATG TGATCTTCT GTCATAAACC

4701 TATCTGCGT CTGCTGAAGC CAGTTACCTT CGGAAAAAGA GTTGGTAGCT CTTGATCCG CAAACAACC ACCGCTGGTA GCGGTGGTTT TTTTGTGTTG  
 ATAGACGCGA GACGACTTCG GTCAATGGAA GCCTTTTCT CAACCATCGA GAACCTAGCC GTTGTGTTGG TGGCGACCAT CGCCACCAA AAAACAAACG

4801 AAGCAGCAGA TTACGCGCAG AAAAAAGGA TCTCAAGAAG ATCCTTTGAT CTTTCTACG GGTCTGACG CTCAGTGGAA CGAAAACTCA CGTTAAGGGA  
 TTCGTGCTCT AATGCGCGTC TTTTCTTCT AGAGTTCTTC TAGGAACTA GAAAGATGC CCCAGACTGC GAGTCACTT GCTTTGAGT GCAATTCCCT

4901 TTTTGGTCAAT GAGATTATCA AAAAGGATCT TCACCTAGAT CCTTTTAAAT TAAAAATGAA GTTTTAAATC AATCTAAAGT ATATATGAGT AAACCTGGTC  
 AAAACCAATA CTCTAATAGT TTTTCTTAGA AGTGGATCTA GGAATTTA ATTTTACTT CAAAATTTAG TTAGATTCA TATATACTCA TTTTGAACCCAG

5001 TGACAGTTAC CAATGCTTAA TCAGTGAGGC ACCTATCTCA GCGATCTGTC TATTTCTGTT ATCCATAGTT GCTGACTCC CCGTCTGTA GATAACTACG  
 ACTGTCAATG GTTACGAAT AGTCACTCCG TGGATAGAT CGCTAGACAG ATAAAGCAAG TAGGTATCAA CCGACTGAGG GGCAGCACAT CTATTGATGC

5101 ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGCGAGA CCCACGCTCA CCGSCTCCAG ATTTATCAGC AATAAACCCAG CCAGCCGGAA  
 TATGCCCTCC CGAATGGTAG ACCGGGTCA CGACGTTACT ATGGCGCTCT GGTGCGAGT GCGCGAGGTC TAAATAGTCG TTATTTGGTC GGTGCGCCTT

5201 GGGCCGAGCG CAGAAGTGGT CCTGCAACTT TATCGCCTC CATCCAGTCT ATTAATTGTT GCGGGGAAGC TAGAGTAAGT AGTTCGCCAG TTAATAGTTT  
 CCGGCTCGC GTCTTACCA GGACGTTGAA ATAGGCGGAG GTAGGTGAGA TAATTAACA CGGCCCTTCG ATCTCATTC TCAAGCGGTC AATTATCAAA

5301 GCGCAACGTT GTTGCCATTG CTGCAGGCAT CGTGGTGTC GCGTCTCGT TTGGTATGGC TTTCATTGAG TCCGGTTCCC AACGATCAAG GCGAGTTACA  
 CCGGTTGCAA CAACGGTAAC GACGTCGTA GCACCACAGT GCGAGCAGCA AACCATACCG AAGTAAGTCG AGGCCAAGG TTGCTAGTTC CGCTCAATGT

5401 TGATCCCCCA TGTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCTCCGAT CAGTGTGAGA AGTAAGTTGG CCGCAGTGT ATCACTCATG GTTATG3CAG  
 ACTAGGGGCT ACAACACGTT TTTTCGCCAA TCGAGGAAGC CAGGAGGCTA GCAACAGTCT TCATTCAACC GCGGTCACAA TAGTGAGTA CAATACCGTC

5501 CACTGCATAA TTCTCTTACT CCGTAAGATG CTTTCTGTG ACTGGTGAGT ACTCAACCAA GTCATTCTGA GAATAGTGA TGCGGCGACC  
 GTGACGTATT AAGAGAATGA CAGTACGGTA GGCATTCTAC GAAAAGACAC TGACCACTCA TGAGTTGGTT CAGTAAGACT CTTATCACAT ACGCCGCTGG

Fig. 8D

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5601 GAGTTGCTCT TGCCCGGGCT CAACACGGGA TAATACCGGC CGCATAGCA GAACCTTAAA AGTCTCATC ATTGGAAAAC GTTCTTCGGG GCGAAAACTC  
CTCAACGAGA ACGGGCCGCA GTTGCCCT ATATGCGC GGTGATCGT CTGAAATTT TCAAGAGTAG TAACCTTTG CAAGAAGCCC CGCTTTGAG

5701 TCAAGGATCT TACCGCTGT GAGATCCAGT TCGATGTAAC CCACTCGTGC ACCCACTGA TCTTCAGCAT CTTTACTTT CACCAGCGTT TCTGGGTGAG  
AGTTCCTAGA ATGGCGACAA CTCTAGGTCA AGCTACATTG GGTGAGCAGG TGGGTGACT AGAAGTCGTA GAAAATGAAA GTGGTCGCAA AGACCCACTC

5801 CAAAAACAGG AAGGCAAAAT GCCGCAAAA AGGAATAAG GCGACACGG AAATGTTGAA TACTCATACT CTTCCCTTTT CAATATTATT GAAGCATTTA  
GTTTTGTCC TTCCGTTTTA CGGCGTTTTT TCCCTATT CCGCTGTGCC TTTACAACCT ATGAGTATGA GAAGGAAAA GTTATAATAA CTTCGTAAT

5901 TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAATGT ATTTAGAAA ATAAACAAAT AGGGGTTCG CGCACATTC CCCGAAAAGT GCCACCTGAC  
AGTCCCAATA ACAGAGTACT CGCTATGTA TAACTTACA TAAATCTTTT TATTGTTTA TCCCAAGGC GCGTGTAAG GGGCTTTTCA CGGTGGACTG

6001 GTCTAAGAAA CCATTATTAT CATGACATTA ACCTATAAA ATAGGCGTAT CACGAGGCC TTTCTCTTC AA (SEQ ID NO: 99)  
CAGATTCTTT GGTAATAATA GTACTGTAAT TGGATATTTT TATCCGCATA GTGCTCCGG AAAGCAGAAG TT

Fig. 8E

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[illegible]

10
20
30  
**F(ab)-12** DIQMTQSPSSLSASVGDRVITITCSASQDISNYLNWYQQ  
**MB1.6** DIQ**IT**QSPSSLSASVGDRVITITCSASQDISNYLNWYQQ  
**H2305.6** DIQ**IT**QSPSSLSASVGDRVITITCSASQDISNYLNWYQQ  
**Y0101** DIQ**IT**QSPSSLSASVGDRVITITCSASQDISNYLNWYQQ  
**Y0192** DIQ**IT**QSPSSLSASVGDRVITIT**RANDICE**SNYLNWYQQ

40
50
60
CDR-L1
70

F(ab)-12 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS  
 MB1.6 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS  
 H2305.6 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS  
 Y0101 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS  
 Y0192 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS

**Fig. 9A**

CDR-L2

F(ab)-12<sup>80</sup> SLQPEDFATYYC<sup>90</sup>QQYSTVPWTFG<sup>100</sup>QGTKVEIKRTV (SEQ ID NO:8)

MB1.6 SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 101)

H2305.6 SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO:103)

Y0101 SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO:105)

Y0192 SLQPEDFATYYC~~QQYSTVPWTF~~GQGTKVEIKRTV (SEQ ID NO: 107)

CDR-L3

F(ab)-12 EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVR  
 MB1.6 EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVR  
 H2305.6 EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVR  
 Y0101 EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVR  
 Y0192 EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVR

CDR-H1

F(ab)-12 QAPGKGLEWVGWINTYTGEPYAADF~~KRRFTFS~~LDTSKSTA

MB1.6 QAPGKGLEWVGWINTYTGEPYAADF~~KRRFTFS~~LDTS~~SNIV~~

H2305.6 QAPGKGLEWVGWINTYTGEPYAADF~~KRRFTFS~~LDTS~~SNIV~~

Y0101 QAPGKGLEWVGWINTYTGEPYAADF~~KRRFTFS~~LDTSKSTA

Y0192 QAPGKGLEWVGWINTYTGEPYAADF~~KRRFTFS~~LDTSKSTA

**Fig. 9B**

			CDR-H2		CDR-7
	80	90	100	110	
F(ab)-12	YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTL	(SEQ ID NO: 7)			
MB1.6	YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTL	(SEQ ID NO: 102)			
H2305.6	YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTL	(SEQ ID NO: 104)			
Y0101	YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTL	(SEQ ID NO: 106)			
Y0192	YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTL	(SEQ ID NO: 108)			
			CDR-H3		

■ = differences from F(ab)-12

10 20 30  
F(ab)-12 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ  
Y0243-1 DIQ■TQSPSSLSASVGDRVTITC■AN■Q■SNYLNWYQQ  
Y0238-3 DIQ■TQSPSSLSASVGDRVTITC■AN■Q■SNYLNWYQQ  
Y0313-1 DIQ■TQSPSSLSASVGDRVTITC■AN■Q■SNYLNWYQQ  
Y0317 DIQ■TQSPSSLSASVGDRVTITCSASODISNYLNWYQQ

CDR-L1

40 50 60 70  
F(ab)-12 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS  
Y0243-1 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS  
Y0238-3 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS  
Y0313-1 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS  
Y0317 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS

Fig. 10A

CDR-L2

80 90 100  
F(ab)-12 SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 8)  
Y0243-1 SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 109)  
Y0238-3 SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 111)  
Y0313-1 SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 113)  
Y0317 SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 115)

CDR-L3

10 20 30  
F(ab)-12 EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVR  
Y0243-1 EVQLVESGGGLVQPGGSLRLSCAASGY■FT■YGMNWVR  
Y0238-3 EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYG■NWVR  
Y0313-1 EVQLVESGGGLVQPGGSLRLSCAASGY■FT■YGMNWVR  
Y0317 EVQLVESGGGLVQPGGSLRLSCAASGY■FT■YGMNWVR

CDR-H1

40 50 60 70  
F(ab)-12 QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA  
Y0243-1 QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA  
Y0238-3 QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA  
Y0313-1 QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA  
Y0317 QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA

Fig. 10B

CDR-H2

80 90 100 110 CDR-7  
F(ab)-12 YLQMNSLRAEDTAVYYCAKYPHYGYGSSHWFYFDVWGQGT (SEQ ID NO: 7)  
Y0243-1 YLQMNSLRAEDTAVYYCAKYPHYGYGSSHWFYFDVWGQGT (SEQ ID NO: 110)  
Y0238-3 YLQMNSLRAEDTAVYYCAKYP■YGYG■SHWFYFDVWGQGT (SEQ ID NO: 112)  
Y0313-1 YLQMNSLRAEDTAVYYCAKYP■YGYG■SHWFYFDVWGQGT (SEQ ID NO: 114)  
Y0317 YLQMNSLRAEDTAVYYCAKYP■YGYG■SHWFYFDVWGQGT (SEQ ID NO: 116)

CDR-H3

0303469.030697

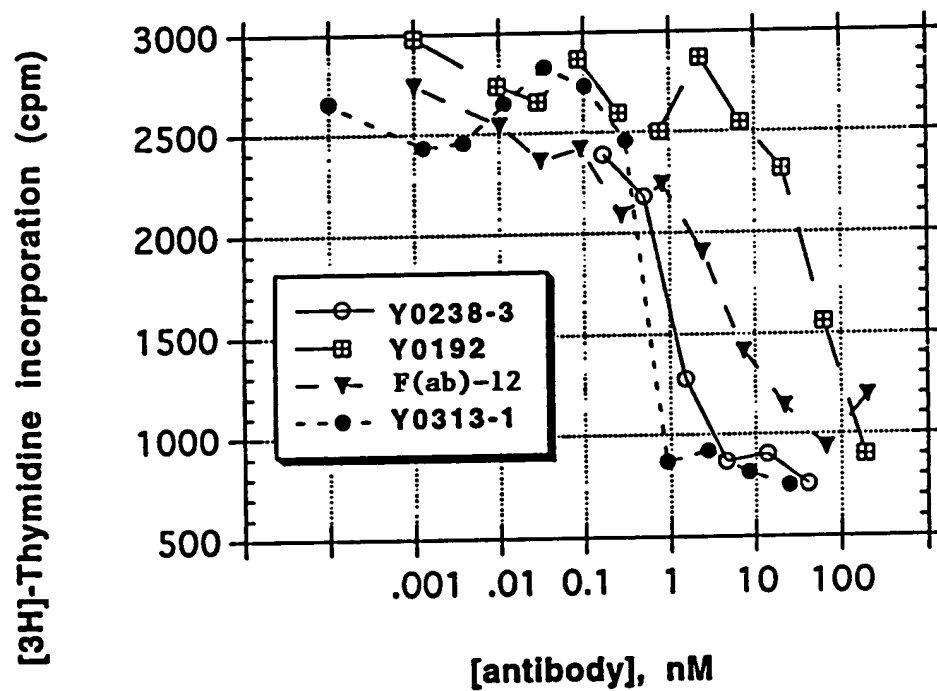


Fig. 11

Fig. 12

